RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 08/252,384 D_____

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RAW SEQUENCE LISTING   DATE: 03/07/2007
PATENT APPLICATION: US/08/252,384D   TIME: 15:04:39

Input Set : N:\efs\03_07_07\08252384D_efs\RACT00100.txt
Output Set: N:\CRF4\03062007\H252384D.raw

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 3 <110> APPLICANT: Reactive Surfaces, Ltd.
 4         McDaniel, Steven
 5         Raushel, Frank M
 6         Wild, James R
 8 <120> TITLE OF INVENTION: Recombinant Organophosphorous Acid Anhydrase and Methods of
Use
10 <130> FILE REFERENCE: TAMK145
12 <140> CURRENT APPLICATION NUMBER: US 08/252,384D
13 <141> CURRENT FILING DATE: 1994-06-01
15 <150> PRIOR APPLICATION NUMBER: US 07/928,540
16 <151> PRIOR FILING DATE: 1992-08-13
18 <150> PRIOR APPLICATION NUMBER: US 07/344,258
19 <151> PRIOR FILING DATE: 1989-04-27
21 <160> NUMBER OF SEQ ID NOS: 4
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1337
27 <212> TYPE: DNA
28 <213> ORGANISM: Pseudomonas diminuta
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (63)..(1160)
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43 Thr Leu Leu Gly Gly Leu Ala Gly Cys Ala Ser Val Ala Gly Ser Ile
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46 ggc aca ggc gat cgg atc aat acc gtg cgc ggt cct atc aca atc tct    203
47 Gly Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile Thr Ile Ser
48                35                  40                  45
50 gaa gcg ggt ttc aca ctg act cac gag cac atc tgc ggc agc tcg gca    251
51 Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala
52             50                  55                  60
54 gga ttc ttg cgt gct tgg cca gag ttc ttc ggt agc cgc aaa gct cta    299
55 Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu
56         65                  70                  75
58 gcg gaa aag gct gtg aga gga ttg cgc cgc gcc aga gcg gct ggc gtg    347
59 Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Ala Gly Val
60 80                  85                  90                  95
62 cga acg att gtc gat gtg tcg act ttc gat atc ggt cgc gac gtc agt    395
63 Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser
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67 Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala
68                115               120               125
70 acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg agg agt gta      491
71 Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val
72                130               135               140
74 gag gaa ctc aca cag ttc ttc ctg cgt gag att caa tat ggc atc gaa      539
75 Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu
76      145               150               155
78 gac acc gga att agg gcg ggc att atc aag gtc gcg acc aca ggc aag      587
79 Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys
80 160               165               170               175
82 gcg acc ccc ttt cag gag tta gtg tta aag gcg gcc gcc cgg gcc agc      635
83 Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser
84                180               185               190
86 ttg gcc acc ggt gtt ccg gta acc act cac acg gca gca agt cag cgc      683
87 Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg
88                195               200               205
90 gat ggt gag cag cag gcc gcc att ttt gag tcc gaa ggc ttg agc ccc      731
91 Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro
92      210               215               220
94 tca cgg gtt tgt att ggt cac agc gat gat act gac gat ttg agc tat      779
95 Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr
96      225               230               235
98 ctc acc gcc ctc gct gcg cgc gga tac ctc atc ggt cta gac cac atc      827
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile
100 240               245               250               255
102 ccg cac agt gcg att ggt cta·gaa gat aat gcg agt gca tca gcc ctc      875
103 Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu
104               260               265               270
106 ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc      923
107 Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu
108               275               280               285
110 atc gac caa ggc tac atg aaa caa atc ctc gtt tcg aat gac tgg ctg      971
111 Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu
112               290               295               300
114 ttc ggg ttt tcg agc tat gtc acc aac atc atg gac gtg atg gat cgc      1019
115 Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg
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118 gtg aac ccc gac ggg atg gcc ttc att cca ctg aga gtg atc cca ttc      1067
119 Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe
120 320               325               330               335
122 cta cga gag aag ggc gtc cca cag gaa acg ctg gca ggc atc act gtg      1115
123 Leu Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly Ile Thr Val
124               340               345               350
126 act aac ccg gcg cgg ttc ttg tca ccg acc ttg cgg gcg tca tga      1160
127 Thr Asn Pro Ala Arg Phe Leu Ser Pro Thr Leu Arg Ala Ser
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132 gtcgcgcatc gatcgatagg catcttcaat ttgatcaggg ctgccacctc caaagccgtg   1280
134 gccacccctg tcgatagtct tgaggacgta gggcacaccg tgcttttcga actgcag        1337
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137 <210> SEQ .ID NO: 2
138 <211> LENGTH: 365
139 <212> TYPE: PRT
140 <213> ORGANISM: Pseudomonas diminuta
142 <400> SEQUENCE: 2

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149             20                  25                  30
152 Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile Thr Ile Ser Glu
153         35                  40                  45
156 Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala Gly
157     50                  55                  60
160 Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu Ala
161 65                  70                  75                  80
164 Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Ala Gly Val Arg
165                 85                  90                  95
168 Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser Leu
169             100                 105                 110
172 Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala Thr
173         115                 120                 125
176 Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val Glu
177     130                 135                 140
180 Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu Asp
181 145                 150                 155                 160
184 Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys Ala
185                 165                 170                 175
188 Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu
189             180                 185                 190
192 Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg Asp
193         195                 200                 205
196 Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro Ser
197     210                 215                 220
200 Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr Leu
201 225                 230                 235                 240
204 Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro
205                 245                 250                 255
208 His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu Leu
209             260                 265                 270
212 Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile
213         275                 280                 285
216 Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu Phe
217     290                 295                 300
220 Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val
221 305                 310                 315                 320
224 Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe Leu
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Output Set: N:\CRF4\03062007\H252384D.raw

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237 <211> LENGTH: 1325
238 <212> TYPE: DNA
239 <213> ORGANISM: Pseudomonas diminuta
242 <220> FEATURE:
243 <221> NAME/KEY: CDS
244 <222> LOCATION: (63)..(1100)
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250    Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Gly Thr
251    1               5               10              15
253 ctg ctc ggc ggc ctg gct ggg tgc gcg acg tgg ctg gat cga tcg gca        155
254 Leu Leu Gly Gly Leu Ala Gly Cys Ala Thr Trp Leu Asp Arg Ser Ala
255             20              25              30
257 cag gcg atc gga tca ata cgt gcg cgt cct atc aca atc tct gaa gcg        203
258 Gln Ala Ile Gly Ser Ile Arg Ala Arg Pro Ile Thr Ile Ser Glu Ala
259             35              40              45
261 ggt ttc aca ctg act cac gag gac atc tgc ggc agc tcg gca gga ttc        251
262 Gly Phe Thr Leu Thr His Glu Asp Ile Cys Gly Ser Ser Ala Gly Phe
263        50              55              60
265 ttg cgt gct tgg cca gag ttc ttc ggt agc cgc aaa gct cta gcg gaa        299
266 Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu Ala Glu
267     65              70              75
269 aag gct gtg aga gga ttg cgc gcc aga gcg gct ggc gtg cga acg att        347
270 Lys Ala Val Arg Gly Leu Arg Ala Arg Ala Ala Gly Val Arg Thr Ile
271 80              85              90              95
273 gtc gat gtg tcg act ttc gat atc ggt cgc gac gtc agt tta ttg gcc        395
274 Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser Leu Leu Ala
275             100             105             110
277 gag gtt tcg cgg gct gcc gac gtt cat atc gtg gcg gcg acc ggc ttg        443
278 Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala Thr Gly Leu
279             115             120             125
281 tgg ttc gac ccg cca ctt tcg atg cga ttg agg tat gta gag gaa ctc        491
282 Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu
283             130             135             140
285 aca cag ttc ttc ctg cgt gag att caa tat ggc atc gaa gac acc gga        539
286 Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu Asp Thr Gly
287     145             150             155
289 att agg gcg ggc att atc aag gtc gcg acc aca ggc aag gcg acc ccc        587
290 Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys Ala Thr Pro
291 160             165             170             175
293 ttt cag gag tta gtg tta aag gcg gcc gcc cgg gcc agc ttg gcc acc        635
294 Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu Ala Thr
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295                   180                   185                        190
297 ggt gtt ccg gta acc act cac acg gca gca agt cag cgc gat ggt gag      683
298 Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg Asp Gly Glu
299                   195                   200                   205
301 cga ggc agg ccg cca ttt ttg agt ccg aag ctt gag ccc tca cgg gtt      731
302 Arg Gly Arg Pro Pro Phe Leu Ser Pro Lys Leu Glu Pro Ser Arg Val
303             210                   215                   220
305 tgt att ggt cac agc gat gat act gac gat ttg agc tat ctc acc gcc      779
306 Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr Leu Thr Ala
307         225                   230                   235
309 ctg ctg cgc gga tac ctc atc ggt cta gac cac atc ccg cac agt gcg      827
310 Leu Leu Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala
311 240                   245                   250                   255
313 att ggt cta gaa gat aat gcg agt gca tca ccg ctc ctg ggc atc cgt      875
314 Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Pro Leu Leu Gly Ile Arg
315                   260                   265                   270
317 tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc atc gac caa ggc      923
318 Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile Asp Gln Gly
319             275                   280                   285
321 tac atg aaa caa atc ctc gtt tcg aat gac tgg ctg ttc ggg ttt tcg      971
322 Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu Phe Gly Phe Ser
323         290                   295                   300
325 agc tat gtc acc aac atc atg gac gtg atg gat cgc gtg aac ccc gac     1019
326 Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val Asn Pro Asp
327         305                   310                   315
329 ggg atg gcc ttc att cca ctg aga gtg atc cca ttc tac gag aga agg     1067
330 Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe Tyr Glu Arg Arg
331 320                   325                   330                   335
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334 Ala Ser His Arg Lys Arg Cys Gln Ala Ser Leu
335                   340                   345
337 tgtgtcaccg acttgcgtgg atgtcacgcc atctggatcc ttccagccag cggccactat   1180
339 tccccgtcaa gataccgaac gatgaagtcg cgcatcgatc gataggcatc ttcaattgtg   1240
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347 <211> LENGTH: 346
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349 <213> ORGANISM: Pseudomonas diminuta
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358             20                  25                  30
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362         35                  40                  45
365 Phe Thr Leu Thr His Glu Asp Ile Cys Gly Ser Ser Ala Gly Phe Leu
366     50                  55                  60
369 Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu Ala Glu Lys
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VERIFICATION SUMMARY   DATE: 03/07/2007
PATENT APPLICATION: **US/08/252,384D**   TIME: 15:04:40

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